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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Tue Aug 14 11:21:10 EDT 2007

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Reviewer Comments:

<210> 1

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer 1

<220>

<221> misc_feature

<222> (1)..(37)

<223> i

<400> 1

aaracnwsna thwsngtnaa rggngarwsn aaygtng

37

The above "<223> i" needs further explanation: what represents i? If "n" represents "i," please state so.

<210> 4

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Fragment 1

Please clarify the above <223> response: "Fragment 1" of which

organism? Please give source of the genetic material. Same error in subsequent sequences.

<210> 12
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> LIC Forward

Please explain the above <223> response: what is the source? Same error in subsequent sequences.

<210> 14
<211> 162
<212> DNA
<213> bee

<220>
<221> misc_feature
<222> (1)..(162)
<223> unknown

Please give the Genus species of the <213> response: per 1.823 of the Sequence Rules, the only valid <213> responses are: the Genus species, "Artificial Sequence," or "Unknown." If "Artificial Sequence" or "Unknown," please explain in the <220>-<223> section.

Please explain the above <223> response. What is unknown? Is "n" unknown? Please clarify.

<210> 15
<211> 54
<212> PRT
<213> bee

<220>
<221> misc_feature
<222> (47)..(47)
<223> The 'Xaa' at location 47 stands for Lys, Asn, Arg, Ser, Thr, Ile,

Met, Xaa, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
Cys, or Phe.

The above <223> response explains that the Xaa at location 47 can represent Xaa; Xaa can only represent a single amino acid: it cannot represent itself.

Also, please give the Genus species of the <213> response.

Application No: 10573794

Version No: 1.0

Input Set:

Output Set:

Started: 2007-08-13 09:43:13.445

Finished: 2007-08-13 09:43:14.442

Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 997 ms

Total Warnings: 13

Total Errors: 2

No. of SeqIDs Defined: 17

Actual SeqID Count: 17

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
E 201	Mandatory field data missing in <223> in SEQ ID (14)
E 201	Mandatory field data missing in <223> in SEQ ID (16)

SEQUENCE LISTING

<110> Suzuki, Koichi
Sakai, Masato

<120> Royal Jelly Peptide and Composition Containing the Same

<130> 2006_0470A

<140> 10573794

<141> 2007-08-13

<150> 10/573,794

<151> 2006-03-28

<150> JP 2003-338665

<151> 2003-09-29

<150> PCT/JP2004/014544

<151> 2004-09-27

<160> 17

<170> PatentIn version 3.1

<210> 1

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer 1

<220>

<221> misc_feature

<222> (1)..(37)

<223> i

<400> 1

aaracnwsna thwsngtnaa rggngarwsn aaygtng

37

<210> 2

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer 2

<400> 2

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29

<210> 3

<211> 29

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer 3

 <400> 3
 tttctgaatt ttattaatta ctttattcg 29

 <210> 4
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Fragment 1

 <400> 4
 aaaacctcta tctctgttaa aggcgaatcc aacgttgatg ttgtttccca 50

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 <211> 40
 <212> DNA
 <213> Artificial Sequence

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 <223> Fragment 2

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 <210> 6
 <211> 40
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Fragment 3

 <400> 6
 gtttctgcag tactgctggc tcagactctg gttaacatcc 40

 <210> 7
 <211> 38
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Fragment 4

 <400> 7
 tgcagatcct gatcgacgct aacgttttcg cttaatag 38

<210> 8
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<212> DNA
<213> Artificial Sequence

<220>
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<400> 8
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<210> 9
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
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<210> 10
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<212> DNA
<213> Artificial Sequence

<220>
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<210> 11
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<212> DNA
<213> Artificial Sequence

<220>
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<400> 11
caattgtagg acgtctagga ctagctgcga ttgcaaaagc gaattatc 48

<210> 12
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> LIC Forward

<400> 12
 ggtattgagg gtcgcaaaac ctctatctct g 31

<210> 13
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> LIC Reverse

<400> 13
 agaggagagt tagagcccta ttaagcgaaa acg 33

<210> 14
 <211> 162
 <212> DNA
 <213> bee

<220>
 <221> misc_feature
 <222> (1)..(162)
 <223> unknown

<220>
 <221> CDS
 <222> (1)..(162)
 <223>

<400> 14
 aaa aca tca atc agt gtc aaa ggc gaa tcg aac gtg gat gtc gtt tcc 48
 Lys Thr Ser Ile Ser Val Lys Gly Glu Ser Asn Val Asp Val Val Ser
 1 5 10 15

caa atc aac agt ttg gtt tca tct atc gtg tct ggt gcc aac gtg tca 96
 Gln Ile Asn Ser Leu Val Ser Ser Ile Val Ser Gly Ala Asn Val Ser
 20 25 30

gca gta ctc cta gct caa act tta gtt aat atc ctg caa att nnn atc 144
 Ala Val Leu Leu Ala Gln Thr Leu Val Asn Ile Leu Gln Ile Xaa Ile
 35 40 45

gac gct aat gtt ttc gct 162
 Asp Ala Asn Val Phe Ala
 50

<210> 15
 <211> 54
 <212> PRT
 <213> bee

<220>
 <221> misc_feature

<222> (47)..(47)
 <223> The 'Xaa' at location 47 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Xaa, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp, Cys, or Phe.

<400> 15

Lys Thr Ser Ile Ser Val Lys Gly Glu Ser Asn Val Asp Val Val Ser
 1 5 10 15

Gln Ile Asn Ser Leu Val Ser Ser Ile Val Ser Gly Ala Asn Val Ser
 20 25 30

Ala Val Leu Leu Ala Gln Thr Leu Val Asn Ile Leu Gln Ile Xaa Ile
 35 40 45

Asp Ala Asn Val Phe Ala
 50

<210> 16
 <211> 162
 <212> DNA
 <213> bee

<220>
 <221> CDS
 <222> (1)..(162)
 <223>

<400> 16
 aaa aca tca atc agt gtc aaa ggc gaa tcg aac gtg gat gtc gtt tcc 48
 Lys Thr Ser Ile Ser Val Lys Gly Glu Ser Asn Val Asp Val Val Ser
 1 5 10 15
 caa atc aac agt ttg gtt tca tct atc gtg tct ggt gcc aac gtg tca 96
 Gln Ile Asn Ser Leu Val Ser Ser Ile Val Ser Gly Ala Asn Val Ser
 20 25 30
 gca gta ctc cta gct caa act tta gtt aat atc ctg caa att ctt atc 144
 Ala Val Leu Leu Ala Gln Thr Leu Val Asn Ile Leu Gln Ile Leu Ile
 35 40 45
 gac gct aat gtt ttc gct 162
 Asp Ala Asn Val Phe Ala
 50

<210> 17
 <211> 54
 <212> PRT
 <213> bee

<400> 17

Lys Thr Ser Ile Ser Val Lys Gly Glu Ser Asn Val Asp Val Val Ser
1 5 10 15

Gln Ile Asn Ser Leu Val Ser Ser Ile Val Ser Gly Ala Asn Val Ser
20 25 30

Ala Val Leu Leu Ala Gln Thr Leu Val Asn Ile Leu Gln Ile Leu Ile
35 40 45

Asp Ala Asn Val Phe Ala
50